## SEQUENCE LISTING

<110> Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING INWARDLY RECTIFYING POTASSIUM CHANNEL (Kir5.1) GENE DISRUPTIONS

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<150> US 60/254,888
<151> 2000-12-11
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ggcagctgta atgtgtactt taaacacatt tttggagaat gggggagcta catggttgat 180
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tacattetet cetggttgat atttggttee atattttgge teatageett teateaegga 300
gacctattaa gcgatccaga tatcacccct tgtgttgaca acgtgcattc atttacggct 360
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Tyr Pro Gly Tyr Pro Pro Glu His Ala Ile Ala Glu Lys Arg Arg Ala
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                                25
Arg Arg Leu Leu His Lys Asp Gly Ser Cys Asn Val Tyr Phe Lys
                            40
His Ile Phe Gly Glu Trp Gly Ser Tyr Met Val Asp Ile Phe Thr Thr
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55

Leu Val Asp Thr Lys Trp Arg His Met Phe Ile Ile Phe Ser Leu Ser

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70
                                         75
Tyr Ile Leu Ser Trp Leu Ile Phe Gly Ser Ile Phe Trp Leu Ile Ala
                                     90
Phe His His Gly Asp Leu Leu Ser Asp Pro Asp Ile Thr Pro Cys Val
                                105
            100
Asp Asn Val His Ser Phe Thr Ala Ala Phe Leu Phe Ser Leu Glu Thr
Gln Thr Thr Ile Gly Tyr Gly Tyr Arg Cys Val Thr Glu Glu Cys Ser
                        135
Val Ala Val Leu Thr Val Ile Leu Gln Ser Ile Leu Ser Cys Ile Ile
                    150
                                         155
Asn Thr Phe Ile Ile Gly Ala Ala Leu Ala Lys Met Ala Thr Ala Arg
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                                     170
Lys Arg Ala Gln Thr Ile Arg Phe Ser Tyr Phe Ala Leu Ile Gly Met
                                 185
Arg Asp Gly Lys Pro Cys Leu Met Trp Arg Ile Gly Asp Phe Arg Pro
                            200
Asn His Val Val Glu Gly Thr Val Arg Ala Gln Leu Leu Arg Tyr Ser
                        215
                                             220
Glu Asp Ser Glu Gly Arg Met Thr Met Ala Phe Lys Asp Leu Lys Leu
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                                         235
Val Asn Asp Gln Ile Ile Leu Val Thr Pro Val Thr Ile Val His Glu
                                     250
                245
Ile Asp His Glu Ser Pro Leu Tyr Ala Leu Asp Arg Lys Ala Val Ala
                                 265
Lys Asp Asn Phe Glu Ile Leu Val Thr Phe Ile Tyr Thr Gly Asp Ser
        275
                            280
                                                 285
Thr Gly Thr Ser His Gln Ser Arg Ser Ser Tyr Ile Pro Arg Glu Ile
                        295
Leu Trp Gly His Arg Phe His Asp Val Leu Glu Val Lys Arg Lys Tyr
                    310
                                        315
Tyr Lys Val Asn Cys Leu Gln Phe Glu Gly Ser Val Glu Val Tyr Ala
                325
                                    330
Pro Phe Cys Ser Ala Lys Gln Leu Asp Trp Lys Asp Gln Gln Leu Asn
            340
                                345
Asn Leu Glu Lys Thr Ser Pro Ala Arg Gly Ser Cys Asn Ser Asp Thr
                            360
Asn Thr Arg Arg Arg Ser Phe Ser Ala Val Ala Val Val Ser Ser Cys
                        375
Glu Asn Pro Glu Glu Thr Val Leu Ser Pro Gln Asp Glu Cys Lys Glu
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                                        395
Met Pro Tyr Gln Lys Ala Leu Leu Thr Leu Asn Arg Ile Ser Met Glu
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Ser Gln Met
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value and sequence

<220> <223> Targeting vector

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